● PRINTER RUSH ●
(PTO ASSISTANCE)

Application : 09/755320	Examiner : Saoud	GAU : 1647
From: lhc/	Location: (IDC) FMF FDC	Date: 1/6/06

Tracking #: 0100 3767   Week Date: 8/15/05

DOC CODE	DOC DATE	MISCELLANEOUS
☐ 1449	_____	☐ Continuing Data
☐ IDS	_____	☐ Foreign Priority
☐ CLM	_____	☐ Document Legibility
☐ IIFW	_____	☐ Fees
☐ SRFW	_____	☐ Other
☐ DRW	_____	
☐ OATH	_____	
☐ 312	_____	
☒ SPEC	_____	

[RUSH] MESSAGE: Sequence listing has never been received electronically. Please take disk containing computer readable form or letter requesting transfer from parent to Mark Spencer in STIC. Thank you.

[XRUSH] RESPONSE: CRF transferred from Parent.

INITIALS: CW

NOTE: This form will be included as part of the official USPTO record, with the Response document coded as XRUSH.

REV 10/04

RAW SEQUENCE LISTING   DATE: 01/26/2006
PATENT APPLICATION: US/09/755,320 TIME: 10:10:26

Input Set : N:\Crf3\RULE60\09755320.raw.txt
Output Set: N:\CRF4\01262006\I755320.raw

SEQUENCE LISTING

```
    3 (1) GENERAL INFORMATION:
    5      (i) APPLICANT: Gorski, David H.
    6                     Walsh, Kenneth
    8     (ii) TITLE OF INVENTION: Growth Arrest Homeobox Gene
   10    (iii) NUMBER OF SEQUENCES: 19
   12     (iv) CORRESPONDENCE ADDRESS:
   13          (A) ADDRESSEE: Calfee, Halter, and Griswold
   14          (B) STREET: 800 Superior Avenue
   15          (C) CITY: Cleveland
   16          (D) STATE: Ohio
   17          (E) COUNTRY: U.S.A.
   18          (F) ZIP: 44114-2688
   20      (v) COMPUTER READABLE FORM:
   21          (A) MEDIUM TYPE: Floppy disk
   22          (B) COMPUTER: IBM PC compatible
   23          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
   24          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
   26     (vi) CURRENT APPLICATION DATA:
C--> 27          (A) APPLICATION NUMBER: US/09/755,320
C--> 28          (B) FILING DATE: 05-Jan-2001
W--> 34          (C) CLASSIFICATION: 435
   31    (vii) PRIOR APPLICATION DATA:
   32          (A) APPLICATION NUMBER: US/08/203,532
   33          (B) FILING DATE: 24-Feb-1994
   36   (viii) ATTORNEY/AGENT INFORMATION:
   37          (A) NAME: Golrick, Mary E.
   38          (B) REGISTRATION NUMBER: 34829
   39          (C) REFERENCE/DOCKET NUMBER: 22311/00114
   41     (ix) TELECOMMUNICATION INFORMATION:
   42          (A) TELEPHONE: (216) 622-8200
   43          (B) TELEFAX: (216) 241-0816
   44          (C) TELEX: 980499
   47 (2) INFORMATION FOR SEQ ID NO: 1:
   49      (i) SEQUENCE CHARACTERISTICS:
   50          (A) LENGTH: 2244 base pairs
   51          (B) TYPE: nucleic acid
   52          (C) STRANDEDNESS: both
   53          (D) TOPOLOGY: linear
   55     (ii) MOLECULE TYPE: cDNA
   57    (iii) HYPOTHETICAL: NO
   59     (iv) ANTI-SENSE: NO
   62     (ix) FEATURE:
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63              (A) NAME/KEY: CDS
64              (B) LOCATION: 197..1108
67     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69 GTCAAGTGTT TATACGTGCA GGAGACTGGC CGCTCGGCTC AGGACTGGGA TTAGCGGGCT        60
71 CTGCTCAAAC CCGCGCGGCT TTTACATTAG GAGTGAGTGG GGGAGAGTCC TAGGATTTCT       120
73 AGTGAAAAGT GACAGCGCTT GGTGGACTTT GGGACCTTCG TGAAGTCTTC TGCTTGGAAG       180
75 CTGAGACTTG CATGCC ATG GAA CAC CCC CTC TTT GGC TGC CTG CGC AGC           229
76                 Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser
77                  1                   5                   10
79 CCC CAC GCC ACA GCG CAA GGC TTG CAC CCC TTC TCG CAG TCT TCT CTG         277
80 Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu
81            15                  20                  25
83 GCC CTC CAT GGA AGA TCT GAC CAC ATG TCC TAC CCC GAA CTC TCC ACA         325
84 Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr
85            30                  35                  40
87 TCT TCC TCG TCT TGC ATA ATC GCG GGA TAC CCC AAT GAG GAG GGC ATG         373
88 Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met
89            45                  50                  55
91 TTT GCC AGC CAG CAT CAC AGG GGG CAC CAC CAC CAC CAC CAC CAC CAC         421
92 Phe Ala Ser Gln His His Arg Gly His His His His His His His His
93 60                  65                  70                  75
95 CAT CAC CAC CAC CAG CAG CAG CAG CAC CAG GCT CTG CAA AGC AAC TGG         469
96 His His His His Gln Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp
97                  80                  85                  90
99 CAC CTC CCG CAG ATG TCC TCC CCG CCA AGC GCG GCC CGG CAC AGC CTT         517
100 His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu
101                 95                  100                 105
103 TGC CTG CAG CCT GAT TCC GGA GGG CCC CCG GAG CTG GGG AGC AGC CCT        565
104 Cys Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro
105             110                 115                 120
107 CCG GTC CTG TGC TCC AAC TCT TCT AGC CTG GGC TCC AGC ACC CCG ACC        613
108 Pro Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr
109             125                 130                 135
111 GGA GCC GCG TGC GCA CCA AGG GAT TAT GGC CGT CAA GCG CTG TCA CCC        661
112 Gly Ala Ala Cys Ala Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro
113 140                 145                 150                 155
115 GCA GAA GTG GAG AAG AGA AGT GGC AGC AAA AGA AAA AGC GAC AGT TCA        709
116 Ala Glu Val Glu Lys Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser
117                 160                 165                 170
119 GAT TCC CAG GAA GGA AAT TAC AAG TCA GAA GTG AAC AGC AAA CCT AGG        757
120 Asp Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg
121                 175                 180                 185
123 AGG GAA AGA ACA GCT TTC ACC AAA GAG CAA ATC AGA GAA CTT GAG GCA        805
124 Arg Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala
125             190                 195                 200
127 GAG TTC GCC CAT CAT AAC TAT CTG ACC AGA CTG AGA AGA TAT GAG ATA        853
128 Glu Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile
129         205                 210                 215
131 GCG GTG AAC CTA GAC CTC ACT GAA AGA CAG GTG AAA GTG TGG TTC CAG        901
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132 Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln
133 220             225                 230                 235
135 AAC AGG AGA ATG AAG TGG AAG CGG GTC AAG GGG GGA CAA CAA GGA GCT       949
136 Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala
137                 240                 245                 250
139 GCA GCC CGA GAA AAG GAA CTG GTG AAT GTG AAA AAG GGA ACA CTT CTT       997
140 Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu
141                 255                 260                 265
143 CCA TCA GAG CTG TCA GGA ATT GGT GCA GCC ACC CTC CAG CAG ACA GGG      1045
144 Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly
145         270                 275                 280
147 GAC TCA CTA GCA AAT GAC GAC AGT CGC GAT AGT GAC CAC AGC TCT GAG      1093
148 Asp Ser Leu Ala Asn Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu
149         285                 290                 295
151 CAC GCA CAC TTA TGATACATAC AGAGACCAGC TCCGTTCTCA GGAAAGCACC          1145
152 His Ala His Leu
153 300
155 ATTGTGATGG CAAATCTCAC CCAAACATCG TTTACATGGC AGATGACTGT GGCAGTGTTG     1205
157 CTTAATATAA TTAAACGCAG GCATCTCAAG TCTGTTTCTC ATGATTGATA GAAGGTTTAC     1265
159 ACTAAGTGCC TCTTATTGAA GATGCTTCCA CAGTGAAATT GGAGAAAGTG AACATATCTA     1325
161 AATATACTTG TTCCTTATAT GACAGAGAGG GAGATGAATG TTTGCTTTGG CTTGCACTGA     1385
163 AAATTAAATT GCTACCAAGA GCAAACTCGG TAAGACATTT TGACTCAAGT TGTCTCCAGA     1445
165 GTGAAGATGT TATAGAAATG CTTTGAACAT TCCAGTTGTA CCAGGTCATG TGTGTGACAC     1505
167 TGGGCAGGTA TTTGCTTTTG CTTGCACTGA AACTTAAACT GCTATCAAGT TAACCCATGA     1565
169 AATAGTTTAT CTTGAACAGC CACAGTGCCT GAAATCACCA AGTGGATATA AAATGAACTG     1625
171 AAATTCTGTA TATATTACTC CTAAGTCATT TTCCTGTCTT CACTAATTTT AGCAAATGCA     1685
173 TTCATATTAG CTGATGAAAA TAGGCTTTCC CGTGGACAAA TGCAGCCAGC TTCTTGTATT     1745
175 TTTATACATT TTTTTGTCAG TCAGAGACAT CAGTATGTGC TTACTTGTGT TCAAGTAGAG     1805
177 GAAATGCAGT AGAGTCTGAT AGGACATATT CTTGGTACCA CAGACAAAAC AAATCTTCTG     1865
179 TTGCATTGAC TATCAACTGC TGCAGATACA TTAGAGAACA CACCTAGCCC CCCTCCAGCC     1925
181 TCCCTCTGTT ATCGCTCGAA GACATTAGCG TCATAGGCAA GTAGTTACCT TGCCAAATGA     1985
183 GTCTTGTGTG GCAGATGTCT GATTTTGTAT CTTTAAACTG TTAATGGTAT GTGTCTGCTT     2045
185 CAGTTAACAG GGAAAAAGAT TTCTTCCTCA TTGTTTATGA TACAAAACCC AAGTGCCAAA     2105
187 CAAAGCTAGT TCTTCAAGGG ATAGATGAGA AACTGAATGT CTGACAAGTA GACTCAGCGA     2165
189 AAATACATTA TTTTTCAGAG GCTGTGTATT CATGCAGTAC AAGTCCTTGT ATTTTGTAAA     2225
191 AAAAAAAGTT AAATAAATG                                                  2244
194 (2) INFORMATION FOR SEQ ID NO: 2:
196       (i) SEQUENCE CHARACTERISTICS:
197           (A) LENGTH: 303 amino acids
198           (B) TYPE: amino acid
199           (D) TOPOLOGY: linear
201      (ii) MOLECULE TYPE: protein
203      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
205 Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro His Ala Thr Ala
206  1             5                  10                  15
208 Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala Leu His Gly Arg
209             20                  25                  30
211 Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Ser Cys
212         35                  40                  45
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Input Set : N:\Crf3\RULE60\09755320.raw.txt
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```
214 Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe Ala Ser Gln His
215     50              55              60
217 His Arg Gly His His His His His His His His His His His Gln
218 65             70              75              80
220 Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp His Leu Pro Gln Met
221             85              90              95
223 Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Gln Pro Asp
224             100             105             110
226 Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser
227         115             120             125
229 Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala
230     130             135             140
232 Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Val Glu Lys
233 145             150             155             160
235 Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Glu Gly
236             165             170             175
238 Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Arg Glu Arg Thr Ala
239             180             185             190
241 Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu Phe Ala His His
242     195             200             205
244 Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala Val Asn Leu Asp
245     210             215             220
247 Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys
248 225             230             235             240
250 Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala Ala Arg Glu Lys
251             245             250             255
253 Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro Ser Glu Leu Ser
254             260             265             270
256 Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp Ser Leu Ala Asn
257     275             280             285
259 Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu His Ala His Leu
260     290             295             300
263 (2) INFORMATION FOR SEQ ID NO: 3:
265     (i) SEQUENCE CHARACTERISTICS:
266         (A) LENGTH: 941 base pairs
267         (B) TYPE: nucleic acid
268         (C) STRANDEDNESS: both
269         (D) TOPOLOGY: linear
271     (ii) MOLECULE TYPE: cDNA
273     (iii) HYPOTHETICAL: NO
275     (iv) ANTI-SENSE: NO
278     (ix) FEATURE:
279         (A) NAME/KEY: CDS
280         (B) LOCATION: 33..941
283     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
285 GTCTTCTACC TGGAACCCGA AACTTGCATG CT ATG GAA CAC CCG CTC TTT GGC         53
286                                    Met Glu His Pro Leu Phe Gly
287                                     1                 5
289 TGC CTG CGC AGC CCT CAC GCC ACG GCG CAA GGC TTG CAC CCG TTC TCC        101
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290 Cys Leu Arg Ser Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser
291          10                  15                  20
293 CAA TCC TCT CTC GCC CTC CAT GGA AGA TCT GAC CAT ATG TCT TAC CCC          149
294 Gln Ser Ser Leu Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro
295     25                  30                  35
297 GAG CTC TCT ACT TCT TCC TCA TCT TGC ATA ATC GCG GGA TAC CCC AAC          197
298 Glu Leu Ser Thr Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn
299 40                  45                  50                  55
301 GAA GAG GAC ATG TTT GCC AGC CAG CAT CAC AGG GGG CAC CAC CAC CAC          245
302 Glu Glu Asp Met Phe Ala Ser Gln His His Arg Gly His His His His
303              60                  65                  70
305 CAC CAC CAC CAT CAC CAC CAT CAG CAG CAG CAG CAC CAG GCT CTG CAA          293
306 His His His His His His His Gln Gln Gln Gln His Gln Ala Leu Gln
307              75                  80                  85
309 ACC AAC TGG CAC CTC CCG CAG ATG TCT TCC CCA CCG AGT GCG GCT CGG          341
310 Thr Asn Trp His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg
311          90                  95                  100
313 CAT AGC CTC TGC CTC CAG CCC GAC TCT GGA GGG CCC CCA GAG TTG GGG          389
314 His Ser Leu Cys Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly
315     105                  110                  115
317 AGC AGC CCG CCC GTC CTG TGC TCC AAC TCT TCC AGC TTG GGC TCC AGC          437
318 Ser Ser Pro Pro Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser
319 120                  125                  130                  135
321 ACC CCG ACT GGG GCC GCG TGC GCG CCG GGG GAC TAC GGC CGC CAG GCA          485
322 Thr Pro Thr Gly Ala Ala Cys Ala Pro Gly Asp Tyr Gly Arg Gln Ala
323              140                  145                  150
325 CTG TCA CCT GCG GAG GCG GAG AAG CGA AGC GGC GGC AAG AGG AAA AGC          533
326 Leu Ser Pro Ala Glu Ala Glu Lys Arg Ser Gly Gly Lys Arg Lys Ser
327              155                  160                  165
329 GAC AGC TCA GAC TCC CAG GAA GGA AAT TAC AAG TCA GAA GTC AAC AGC          581
330 Asp Ser Ser Asp Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser
331          170                  175                  180
333 AAA CCC AGG AAA GAA AGG ACA GCA TTT ACC AAA GAG CAA ATC AGA GAA          629
334 Lys Pro Arg Lys Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu
335     185                  190                  195
337 CTT GAA GCA GAA TTT GCC CAT CAT AAT TAT CTC ACC AGA CTG AGG CGA          677
338 Leu Glu Ala Glu Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg
339 200                  205                  210                  215
341 TAC GAG ATA GCA GTG AAT CTG GAT CTC ACT GAA AGA CAG GTA AAA GTC          725
342 Tyr Glu Ile Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val
343              220                  225                  230
345 TGG TTC CAA AAC AGG CGG ATG AAG TGG AAG AGG GTA AAG GGT GGA CAG          773
346 Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln
347              235                  240                  245
349 CAA GGA GCT GCG GCT CGG GAA AAG GAA CTG GTG AAT GTG AAA AAG GGA          821
350 Gln Gly Ala Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly
351              250                  255                  260
353 ACA CTT CTC CCA TCA GAG CTG TCG GGA ATT GGT GCA GCC ACC CTC CAG          869
354 Thr Leu Leu Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln
```

VERIFICATION SUMMARY   DATE: 01/26/2006
PATENT APPLICATION: US/09/755,320   TIME: 10:10:27

Input Set : N:\Crf3\RULE60\09755320.raw.txt
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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:34 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)